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TECH CENTER 1600/2900

1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/262,126C

DATE: 04/18/2001
TIME: 11:17:36

Input Set : A:\GC396-2-seqlist.txt
Output Set: N:\CRF3\04182001\I262126C.raw

ENTERED

3 <110> APPLICANT: Miller, Brian S.
4 Shetty, Jayarama K.
6 <120> TITLE OF INVENTION: Modified Forms of Pullulanase
9 <130> FILE REFERENCE: GC396-2
11 <140> CURRENT APPLICATION NUMBER: 09/262,126C
12 <141> CURRENT FILING DATE: 1999-03-03
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2794
20 <212> TYPE: DNA
21 <213> ORGANISM: Bacillus deramificans
23 <220> FEATURE:
24 <221> NAME/KEY: misc_feature
25 <222> LOCATION: (1)...(2794)
26 <223> OTHER INFORMATION: n = A, T, C, or G
28 <400> SEQUENCE: 1
29 gatgggaaca cgacaacgat cattgtccac tatttttgcc ctgctggtga ttatcaacct 60
30 tggagtctat ggatgtggcc aaaagacgga ggtggggctg aatacgattt caatcaaccg 120
31 gctgactctt ttggagctgt tgcaagtgt gatattccag gaaacccaag tcaggtagga 180
32 attatcgctt gcactcaaga ttggacaaa gatgtgagcg ctgaccgcta catagattta 240
33 agcaaaaggaa atgaggtgtg gctttagaa ggaacagcc aaatttttta taatgaaaaa 300
34 gatgctgagg atgcagctaa acccgctgta agcaacgctt atttagatgc ttcaaaccag 360
W--> 35 gtgctgggta aacttagcca gccgttaact cttggggaag gnnnaagcgg ctttacggtt 420
36 catgacgaca cagcaataa ggatattcca gtgacatctg tgaaggatgc aagtcttgg 480
37 caagatgtaa ccgctgtttt gccaggtacc ttccaacata tttttggagg ttccgattgg 540
38 gcacctgata atcacagtac tttattaaaa aaggtgacta acaatctcta tcaattctca 600
39 ggagatcttc ctgaaggaaa ctaccaatat aaagtggctt taaatgatag ctggaataat 660
40 ccgagttacc catctgacaa cattaattta acagtccctg ccggcgggtg acacgtcact 720
41 ttttcgtata ttccgtccac tcatgcagtc tatgacacaa ttaataatcc taatgcggat 780
42 ttacaagtag aaagcggggt taaaacggat ctctgacgg ttactctagg ggaagatcca 840
43 gatgtgagcc atactctgtc cattcaaaca gatggctatc aggcaaagca ggtgatacct 900
44 cgtaattgtg ttaattcatc acagtactac tattcaggag atgatcttgg gaatacctat 960
45 acacagaaaag caacaacctt taaagtctgg gcaccaactt ctactcaagt aaatgttctt 1020
46 ctttatgaca gtgcaacggg ttctgtaaca aaaatcgtag ctatgacggc atcgggccat 1080
47 ggtgtgtggg aagcaacggt taatcaaaac cttgaaaatt ggtattacat gtatgaggta 1140
48 acaggccaag gctctaccgg aacggctgtt gatccttatg caactgcatg tgcaccaa 1200
49 ggaacgagag gcatgattgt ggacctggct aaaacagatc ctgctggctg gaacagtat 1260
50 aaacatatta gcgcaaaagaa tatagaagat gaggtcatct atgaaatgga tgtccgtgac 1320
51 ttttccattg accctaattc gggatgaaa aataaaggga agtatttggc tcttacagaa 1380
52 aaaggaacaa agggccctga caacgtaaag acggggatag attccttaaa acaacttggg 1440
53 attactcatg ttcagcttat gcctgttttc gcatctaaca gtgtcgatga aactgatcca 1500
54 acccaagata attgggggta tgacctcgc aactatgatg ttccggaagg gcagtatgct 1560
55 acaaatgcga atggtaatgc tcgtataaaa gagttaaagg aaatggttct ttcactccat 1620
56 cgtgaacaca ttgggggttaa catggatgtt gcttataatc ataccttgc cacgcaaatc 1680
57 tctgacttcg ataaaattgt accagaatat tattaccgta cgatgatcca ggtaattata 1740
W--> 58 ccaacggatc aggtactgga aatgaaattg cangcngaaa ggccaatggt tcaaaaattt 1800

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59 attattgatt cccttaagta ttgggtcaat gagtatcata ttgacggctt ccgttttgac 1860
60 ttaatggcgc tgcttgaaa agacacgatg tccaaagctg cctcggagct tcatgctatt 1920
61 aatccaggaa ttgcacttta cggtagacca tggacgggtg gaacctctgc actgccagat 1980
62 gatcagcttc tgacaaaagg agctcaaaaa ggcattgggag tagcgggtgtt taatgacaat 2040
63 ttacgaaacg cgttggacgg caatgtcttt gattcttccg ctcaagggtt tgcgacaggt 2100
64 gcaacaggct taactgatgc aattaagaat ggcgttgagg ggagtattaa tgactttacc 2160
65 tcttcaccag gtgagacaat taactatgtc acaagtcagt ataactacac cctttgggac 2220
66 aaaatagccc taagcaatcc taatgattcc gaagcggatc ggattaaaaat ggatgaactc 2280
67 gcacaagcag ttgttatgac ctcaacaaggc gttccattca tgcaaggcgg ggaagaaatg 2340
W--> 68 cttcgtanaa aaggcggcaa cgacaatagt tataatgcag gcgatgcggt caatgagttt 2400
69 gattggagca ggaaagctca atatccagat gttttcaact attatagcgg gctaattccac 2460
70 cttcgtcttg atcaccacagc cttccgcagt acgacagcta atgaaatcaa tagccaccctc 2520
71 caattcctaa atagtccaga gaacacagtg gcctatgaat taactgatca tgtaataaaa 2580
72 gacaaatggg gaaatatcat tgttgtttat aacccaaata aaactgtagc aaccatcaat 2640
73 ttgccgagcg gaaaatgggc aatcaatgct acgagcggta aggtaggaga atccaccctt 2700
74 ggtcaagcag agggaaagtg ccaagtacca ggtatatcta tgatgatcct tcatcaagag 2760
75 gtaagcccag accacggtaa aaagtaatag aaaa 2794
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 956
79 <212> TYPE: PRT
80 <213> ORGANISM: Bacillus deramificans
82 <220> FEATURE:
83 <221> NAME/KEY: VARIANT
84 <222> LOCATION: (1)...(956)
85 <223> OTHER INFORMATION: Xaa = Any Amino Acid
87 <400> SEQUENCE: 2
88 Met Ala Lys Lys Leu Ile Tyr Val Cys Leu Ser Val Cys Leu Val Leu
89 1 5 10 15
90 Thr Trp Ala Phe Asn Val Lys Gly Gln Ser Ala His Ala Asp Gly Asn
91 20 25 30
92 Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln
93 35 40 45
94 Pro Trp Ser Leu Trp Met Trp Pro Lys Asp Gly Gly Ala Glu Tyr
95 50 55 60
96 Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala Ser Ala Asp
97 65 70 75 80
98 Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp
99 85 90 95
100 Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly
101 100 105 110
102 Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe Tyr Asn Glu
103 115 120 125
104 Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu
105 130 135 140
106 Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu
107 145 150 155 160
W--> 108 Gly Glu Gly Xaa Ser Gly Phe Thr Val His Asp Asp Thr Ala Asn Lys
109 165 170 175
110 Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val

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```

111          180          185          190
112 Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp
113          195          200          205
114 Trp Ala Pro Asp Asn His Ser Thr Leu Leu Lys Lys Val Thr Asn Asn
115          210          215          220
116 Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr Lys
117 225          230          235          240
118 Val Ala Leu Asn Asp Ser Trp Asn Asn Ser Tyr Pro Ser Asp Asn Ile
119          245          250          255
120 Asn Leu Thr Val Pro Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile
121          260          265          270
122 Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro Asn Ala Asp
123          275          280          285
124 Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu
125          290          295          300
126 Gly Glu Asp Pro Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly
127 305          310          315          320
128 Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val Leu Asn Ser Ser Gln
129          325          330          335
130 Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala
131          340          345          350
132 Thr Thr Phe Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu
133          355          360          365
134 Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr Lys Ile Val Pro Met Thr
135          370          375          380
136 Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu
137 385          390          395          400
138 Asn Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr
139          405          410          415
140 Ala Val Asp Pro Tyr Ala Thr Ala Ile Ala Pro Asn Gly Thr Arg Gly
141          420          425          430
142 Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp
143          435          440          445
144 Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val Ile Tyr Glu Met
145          450          455          460
146 Asp Val Arg Asp Phe Ser Ile Asp Pro Asn Ser Gly Met Lys Asn Lys
147 465          470          475          480
148 Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys Gly Pro Asp Asn
149          485          490          495
150 Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Gly Ile Thr His Val
151          500          505          510
152 Gln Leu Met Pro Val Phe Ala Ser Asn Ser Val Asp Glu Thr Asp Pro
153          515          520          525
154 Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr Asp Val Pro Glu
155          530          535          540
156 Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys Glu Phe
157 545          550          555          560
158 Lys Glu Met Val Leu Ser Leu His Arg Glu His Ile Gly Val Asn Met
159          565          570          575

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```

160 Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile Ser Asp Phe Asp
161                               580                               585                               590
162 Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile
163                               595                               600                               605
W--> 164 Pro Thr Asp Gln Val Leu Glu Met Lys Leu Xaa Ala Glu Arg Pro Met
165                               610                               615                               620
166 Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr Trp Val Asn Glu Tyr
167                               625                               630                               635                               640
168 His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp
169                               645                               650                               655
170 Thr Met Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile
171                               660                               665                               670
172 Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
173                               675                               680                               685
174 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
175                               690                               695                               700
176 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
177                               705                               710                               715                               720
178 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
179                               725                               730                               735
180 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
181                               740                               745                               750
182 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
183                               755                               760                               765
184 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
185                               770                               775                               780
186 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
187                               785                               790                               795                               800
W--> 188 Phe Met Gln Gly Gly Glu Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
189                               805                               810                               815
190 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
191                               820                               825                               830
192 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
193                               835                               840                               845
194 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
195                               850                               855                               860
196 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
197                               865                               870                               875                               880
198 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
199                               885                               890                               895
200 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
201                               900                               905                               910
202 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
203                               915                               920                               925
204 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
205                               930                               935                               940
206 Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys
207                               945                               950                               955
209 <210> SEQ ID NO: 3

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DATE: 04/18/2001

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Input Set : A:\GC396-2-seqlist.txt

Output Set: N:\CRF3\04182001\I262126C.raw

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210 <211> LENGTH: 718
211 <212> TYPE: PRT
212 <213> ORGANISM: Bacillus subtilis
214 <400> SEQUENCE: 3
215 Met Val Ser Ile Arg Arg Ser Phe Glu Ala Tyr Val Asp Asp Met Asn
216 1 5 10 15
217 Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
218 20 25 30
219 Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
220 35 40 45
221 Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
222 50 55 60
223 His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
224 65 70 75 80
225 His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
226 85 90 95
227 Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
228 100 105 110
229 Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
230 115 120 125
231 Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
232 130 135 140
233 Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
234 145 150 155 160
235 Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
236 165 170 175
237 Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
238 180 185 190
239 Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
240 195 200 205
241 Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
242 210 215 220
243 Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
244 225 230 235 240
245 Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Ser Gly
246 245 250 255
247 Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
248 260 265 270
249 Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
250 275 280 285
251 Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
252 290 295 300
253 Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
254 305 310 315 320
255 Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
256 325 330 335
257 Val Phe Asn His Val Tyr Lys Arg Glu Asn Ser Pro Phe Glu Lys Thr
258 340 345 350
259 Val Pro Gly Tyr Phe Phe Arg His Asp Glu Cys Gly Met Pro Ser Asn

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VERIFICATION SUMMARY

DATE: 04/18/2001

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TIME: 11:17:37

Input Set : A:\GC396-2-seqlist.txt

Output Set: N:\CRF3\04182001\I262126C.raw

L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

STATISTICS SUMMARY

DATE: 04/18/2001

PATENT APPLICATION: US/09/262,126C

TIME: 11:17:37

Input Set : A:\GC396-2-seqlist.txt

Output Set: N:\CRF3\04182001\I262126C.raw

Application Serial Number: US/09/262,126C

Alpha or Numeric: Numeric

Application Class:

Application File Date: 03-03-1999

Art Unit: 1652

Software Application: FastSeq

Total Number of Sequences: 9

Total Nucleotides: 2794

Total Amino Acids: 2795

Number of Errors: 0

Number of Warnings: 6

Number of Corrections: 0

MESSAGE SUMMARY

341 W: 6 ((46) "n" or "Xaa" used)